

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT
CCAGAAAACAACCCCTTTTGGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWFFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFFGFFLT YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCTTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCACTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCGTGATCCTGG
TTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTC
CATTTCTAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAACCGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTGGTCCCAACACATTTCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCCGTGCTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAAGCTTAAAGCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA
GATATAAGAGGGGGGAAAATGGAACCGGGCTGACATTTTATAAACAAACAAAATGCTATGGTAGC
ATTTTTCACCTTCATAGCATACTCCTTCCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTTACATGGAAAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTTAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV
LNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFFWKLGD
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTIIQQEVDLEELSRQ
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKEFFYAISSSKSSNVIVLLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAKHQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAATCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTTCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGTGCATCTCTAG
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAAGTCTGCTGCATTCCAGAA
 ATTATCACCACCAAGATCCCATATTCAACACTCAAAGTGCACACAAACAGAAATTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTTATG
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAGCAGCATTCAAGAAATGA
 AGCTGCTGGGTTTGGAGGTGTCCCGACGGCTCTGCTAGTGTCTGCTCTCCTCTTCTTTGTGTG
 CAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT
 CAGCAGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCATA
 TGAGGAATCAAAGAAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC
 GATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT
 CATGCTCCTTACCCTGCCCGAGCTGGGGAAATCAAAGGGCCAAAGAACCAGAAAGAAAGTCCA
 CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCT
 TTCTAGCCTGGCTATGTCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGAAGGAC
 CTAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA
 GCTCTGAAAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCCGTAAGAGCAAAAGAAT
 GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTCTTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
 CTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGTGTGCAAGGTATTACACTCTGAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAACTAAT
 TTTTATTTTGTGCTGAGCTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTCCAAAGAAGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

FIGURE 6

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTTPPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFPFPTNKNQQKEMIETKVVKEEKANDSNPNNEESKKT DKNPEESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCCGGG
GGCCTCCCGGGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCGGGGCGG
CGGCTGCGGGGCGCAGAGCGGAGATCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCCG
GCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAAATGAGACCAACACAGAC
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGCTGTGGAGACCA
GCTGTGTGTCTGGGGTCACTGCACCAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC
ACACCCCTGCCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCAGAGAGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTCTCTA
CATCTTCTTCCAGTAAGTTTCCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTCAGCT
CCCCCAGGCTGTTCTCAGGCTTCACAGTCTGGTGTGCTTGGGAGAGTCAGGCAGGGTTAACTGCA
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTTGGAGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC
TGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCTGCTTTGCAAACATCAACCTGGCAAAAATG
CAACAAATGAATTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTGCG
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA
CTACTGTTAGGAACAGCAGTGTTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTAAATATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEAAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRDSECCGDQLCVWGHC
TKMATRGSNGTICDNQRDCQPGGCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG
ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE
RSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCAAAG
GCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTTGGGGCTCTTCTGGACCTT
AACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCAATTGGCATTGAGGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGGTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCCTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
ATTGTGAGGGTGGTCTGCTGGACAAAGTACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGGTCTGTCTTCTTTTTTTTCTCCGGTCGCATCCCGGGGTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCCTGGGGGCCTAT
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCACCCCAACGTCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA
AAGATTTTATTAAAGATATTTTGTTAACCTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEFWTL
NWVLALGQCVLGAFASFYWAFHKPDIFTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
IVRVVLDKVTDLLLFFGKLLVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCCCCGCGCCCGGCGCCGGCGCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC
TCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGTGCTGCCCCGC
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCCTGGGGGTGCTGGTGTCCA
TCATTATGCTGAGCCCGGCGTGGAGAGTCAGTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC
GGGATCCCCACCGTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
CATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTTTCACCCTGCTCATGCTCTGCGTGAGCAGCA
GCCGGGACCCCCGGGCTGCCATCCAGAATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC
ACCGTGGGTGCCCTTCTACATCCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGGG
CTCCTTCTCTTCATCCTCATCCAGTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGT
GGCTGGGCAAGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAAGGCCTCTTCTTCTCACTCTCCTC
TTCTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGTGCCA
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGTCTCTGC
CCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTATCACCCCTACACCATG
TTTGTCACTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
TGGGCCTCATCATCTTCTCTCTGTGCACCCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGT
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
ACTTCTGCCTGGTGTGCGCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG
ACCCGGAAGATGATCAGCACGTGGACCGCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
CCTCTACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCTCA
CAGCCTGCCATCTGGTGCCCTCCTGCCACCTGGTGCCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCCCTGAGCCGGGC
CTTCTAGTCGTAGTGCCCTTCAAGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
ACCCACACGGTGGAGCTGCCTCTTCCCTTCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCACACAG
TGGGGCATCCGGCACTGAAGCCCTGGTGTCTCCTGGTCACGTCCCCAGGGGACCTGCCCCCTTCTG
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTCTAATAAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 12

MGACLGACSLLSASCCLCGSAPCILSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL
YKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVCSIAAVLPKV
QDAQPNSSGLLQASVITLYTMFVTWSALSSIQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVITYSY
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTTGTACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG
ACTGCCCAATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTCATTCATC
CTTGCCCTGGATTGAGACGTGGTTCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTCAC
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGATTCTTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAGTGAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTTCAGCCAATTTCAATTAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLLWIIELNVNGGIENTLEKEVMQYDIYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQEAEEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG
 CCGCGGCTGCCCCGGCTCCCTGCGCCGCGCCCTCCCGGACAGAAGATGTGCTCCAG
 GGTCCCTCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGACGGGTGCCAT
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCC
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
 AGGCAGCTTTGCCGGCTGCCGGGCTGCAGTCTCTGGACCTGTCACAGAACCAGATCGCCAGCC
 TGCCCGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
 CATGAAATCACCAATGAGACCTTCCGTGGCTGCGGCGCCTCGAGCGCCTTACCTGGGCAAGAA
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
 AGGACAACGAGCTGCGGGCACTGCCCGCTGCGCCTGCCCGCCTGCTGCTGCTGGACCTCAGC
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACCTGGAGGCGCTGCGGCT
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTACGCCGCTTGCGCAACCTCCACGACC
 TGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCTGACG
 CGCCTGCGGCTGGCCGGCAACACCCGCTTGGCCAGCTGCGGCGCGAGGACCTGGCCGGCTGGC
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGC
 TGGTTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGTGCCA
 CTTCCCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGTGCCAG
 CCACCACCACACAGCCACAGTGCCACCACGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCT
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCTC
 CACTGCCCCACGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
 ATGGGGGCACATGCCACCTGGGGACACGGCACCTGGCGTGCTTGTGCCCCGAAGGCTTACG
 GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAG
 GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGCGGCTGC
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACAGGTCACCCA
 GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCGGGCGGGTGCCGAGG
 GCGAGGAGGCTGCGGGGAGGCCATACACCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
 CAGGCCCGGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
 GCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGGCGGCCATGGCAGCAGCGGCTCAGG
 ACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTCCCCTTGGAG
 CCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
 ACTCATGGGCTTCCAGGGCCTGGCCTCCAGTACCCCTCCAGCAAGCCCTACATCTAAGCCA
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGACAGAGGGCTGTGTGACCACAGCT
 GGGCCCTGTTCCTCTGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
 CTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
 CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGTCTGCTGGGCTCTCCAC
 TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGC
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCAAGGAACAAAAGAACTGGAAAGGAAGATGC
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCATTTATCT
 GGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGAAGACAAACGATGATATGAA
 GGCCTTTTGAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVP LLLPL LLL L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
A L R L A G L G L Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q G T R P S P T P
V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y
T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
L L A A L A A V G A A Y C V R R G R A M A A A Q D K Q V G P G A G P L E L E G V K V P L E P G P K A T E G G E A L P S G S E
C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCTCGG
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTAGAAGAATCTGA
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAG
AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAATCCTTAATGGAAG
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTGGTGATTACTTGCCACAGAATATCCAG
GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG
CTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGATATTATACAT
TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTTAGTGGGAAGGCT
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGCCACAACCTTTTCAGCTTTTCATGATC
CAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACCTCCTTCAAATCTTGTTAATGGATAT
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTCTTTAAATGATTAG
TTTGGCTGATTGCCCCATAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTCTCTGAGTTG
GAATTGTCAGAATCATTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA
AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTGCAACAATGC
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTCTG
TTTTTTACTTTTCATGATTGGCTGTCTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG
AAGATTAATCATTTTTAATAAAATTTATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 18

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSESVKDHTTAGRVVAGQIFLDSESESEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHPFLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKKGFCETEEEEAAKRQMQEAEMMYQTGMKIINGSNKKSQKR
EAYRYLQKAASMNHTKALERSYALLFGDYL PQNIQAAREMF EKLTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTFGALGGNLI AHMVLVSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAAGCCATTCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTCTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACCTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGT
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCAGCTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCATTCCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKG FHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK
AFGVHVSCIEPGLFKTNLADPVKVIKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMD
LSPVVECMDHALTSLEPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTGCGCGGTGCTCTCGGGCTTTGTGCTCGGCG
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
CATTAGAAATATATTCATGCTATCAGCTTTTGTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATCCGT
CGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTTGCAGGAGCATTT
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
ATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTACAGGGTACCTTTAGTGGTT
GCCAATCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA
GAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA
ACATTTTTCTTTGTGACGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTCTGTGTT
ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACTACAACCACCATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC
AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA
GATACACAAGACAAACGATCTAAAGCAAATACCTGGTAGTAGTAACCAAGATAAAGCATCCAAAAT
GAGCAGCCCAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
CTACATTTGATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTCATTTGTTTTTACTATGTTCAAC
TGTTTGACAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
ACACATTCTTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
GAGACCATGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTATTTTCAAATATGGAAG
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
AAAATTTAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLVDVNDLTL
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLDQTQDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA
 GCAGCGCGCAGCGAACGCCCGCGCGCCGCCACACCCCTCTGCCGTCCCCGCGGCGCCTGCCACCCTTCCCTCCTTCCCC
 GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTGCTGCCCGCGGAAACCCCGAGGTACACAGCCCGCGCCTCT
 GCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGGCGCCTGGCACCGGGGACCGTTGCCTGA
 CGCGAGGCCAGCTCTACTTTTCGCCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACTCCAACCTCCTTCTCCC
 TCCAGCTCCACTCGTAGTCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCCGCTTCCCGTCCGGTCCCAAA
 GGTGGGAACGCGTCCGCCCCGCGCCGACCATGGCACGGTTGCGCTTCCCGCGCTTCTCTGCACCCTGGCAGTGCTC
 AGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGACGCTTTTACGTGTCCAAAGGCTTC
 AACAGAAGCATGCCCCCTCCACGAGATCAACGGTGATCATTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT
 CAAGAGATGGAGGAGAAGTACAGCCTGCAAGTAAGATGATTCAAAGTGTGGTCAGCGAACAGTGAATCATTG
 CAAGCTGTCTTTGCTTACGTTACAAGAAGTTTATGAATTTCTCAAAGAACTACTTGAAATGCAGAGAAATCCCTG
 AATGATATGTTTGTGAAGACATATGGCCATTATACATGCAAAATCTGAGCTATTTAAAGATCTCTCGTAGAGTTG
 AAACGTTACTACGTGGTGGGAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG
 TTCCGCTGCTGAACCTCCAGTACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGAGCAGCTGAAG
 CCCTTCGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGCTACTTTCTGCTCAAGGC
 TTAGCGGTTGCGGGAGATGCTGAGCAAGGTTCCGTTGTAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG
 ATGATCTACTGCTCCACTGCCGGGCTCTCGTACTGTGAAGCATGTTTACAACACTGCTCAAACATCATGAGAGGC
 TGTTTGGCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
 GAGGGTCTCTTCAACATTGAATCGGTGATGATCCCATGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
 AATAGTGTTCAGTGTCTCAGAAGGTTTTCAGGGATGTGGACCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
 TCCATCTCTGAAAGTGCCCTTCAGTGTCTCGCTTCCAGCCACATCACCCGAGGAACGCCCAACACAGCAGCTGGCACT
 AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCTTCCGAGCAAC
 GTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
 CTGTTTGCACTGACAGGAAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAACACAGAC
 ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
 GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
 TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGTGGTGTCCGTCTGGGGCA
 CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTCTCTGTTATGAGAGAGTGGAGATTAATTTCTCAAACCTCTGAG
 AAAAAGTGTTCATCAAAAAGTTAAAGGCACCACTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA
 TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTAGTTTGGG
 AGGAAAAGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
 CTATAGTTAGTTGTGCATTGTGATTTTATCACTCTATTATTGTTTGTATGTTTTTTCTCATTTCGTTTGTGGGTT
 TTTTTTCCAACGTGATCTCGCCTTGTTCCTTACAAGCAACAGGGTCCCTTCTGGCACGTAACATGTACGTATT
 TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRL
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFGCGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSSLPSNVCNDERMAAGNGNEDDCWNGKGSRYLFAVTGNGLANQGNNPEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT
AGCTAGTGTCATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQCPCDHFKNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAGCTACTTCCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTG
CTCTGTGCAGAGCCCAAGGAAGTCTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTC
GAGCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA
GCAGAATGAGAGAAGACATTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC
CCAATGTTGTCCCTTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTLP LHL MALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQIKGL
TGASGKVALLELGCGTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRLRPGGVLFFWEHVAEPYGSWAFMWQQVFEPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFSSKALICSFPSL
QLEQATHQPIYLPLRGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32.

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCAATTAAGAAATT
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPAMPATCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGAATCATGTCGG
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
TTCAGATTCATCACCACCCCTTCTGGTTCACATTTTCATTTTATTGTTATTTTGGGATTGTTGTT
TGCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCCAGGTT
ATGGAAGGCGGCCAAGTGAATATAAGCCCTTTTCGGGCATTCCGTACATGTGGTCTGACCATTT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
TGGTTACTTGTATTTC AACAGAAGTAAAAATGATCCTCCTGATCATCCATCCTTTCTGCTCTC
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG
GATTCCGAGAATCATTGTCATGTACATGCAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAAGTCTATTAATGGGACAGATTCTGTACATCAGCAAAAGATGC
ATTCAAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAAC
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC
TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
TTAAAAGACCTAATAAACCTATTCTTCTCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDLSIE
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA
GAVVTCYFNRSKNPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFSLVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFSLFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCTTAGA
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT
 GAAAATTTTGTGAAAAAAATTCCTTCTTCAAACAAGGGTGTCTTCTGATATTTATGAGGAC
 TGTGTGTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTTGCTGGTGAAGTAC
 ATTCAAACAAAGAAACGGCAAAGAAGATTAAAGGCCCAAGTTCACTGTGCCTCAGATCAACTGC
 GATGTCAAAGCCGGAAGATCATCGATCCTGAGTTTATTGTGAAATGTCCAGCAGGATGCCAAGA
 CCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG
 TACACAGTGGTGTGCTTGATAATTCAAGAGGGAAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT
 GGTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCAC
 CACCTTGCCAAGGCCATCCCCTTCTGCTGCTTACCACCAGCATCCCAGACCACAATCAGTGG
 GCCACAGGAGCCAGGAGATGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCC
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC
 GGATGTCAAGCTGGGACTTGTTCAAAAGAAGATTGAGCACACAGTCTTTGGAGCCAGTATCCC
 TGGGAGATCCAAACTGCAAAATTGACTTGTCTGTTTTAATTGATGGGAGCACCAGCATTGGCAAA
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGC
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCCTGCTACTCACTTTAACCTCAAGACAC
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT
 GTAGGTCGGGCCATCTCCTTTGTGACCAAGAATCTTTTCCAAAGCCAATGGAACAGAGCGG
 GGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 GACTTGGGAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGAAAAATGAG
 AAGCAGTATGTGGTGGAGCCCAACTTTGCAAAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC
 GCTCCACGTGCAGAGCTGGTTTGGCCCTCCACAAGACCCTGCAGCCTCTGGTGAAGCGGGTCTGCG
 AACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAAGTGGCTGACATTGGCTTCGTATCGAC
 GGCTCCAGCAGTGTGGGGACGGGCACTTCCGCACCGTCCCTCCAGTTTGTGACCAACCTCACCA
 AGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC
 TGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC
 TACTGGAGTGGTGGCACCAGCACGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA
 GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCAGCGGGAGGTCTACGACGACGTCC
 GGATCCCAGCCATGGCTGCCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCTGGGCT
 GCCCAAGAGGAGCTAGAAGTCATTGCCACTCACCCGCCAGAGACCACTCCTTCTTGTGGACGA
 GTTTGACAACTCCATCAGTATGTCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC
 AGCCTCGGAACGAATTCAAGCAGGCAGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTT
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC
 AAATGTCTTGTATTATCTTTGCCATCATGCTTTTTCATATTCCAAACTTGAGTTACAAAGA
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT
 TTTGACAATTGTTTTCAAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG
 AGCTTTTGTGAGATTTTTAAGTTGTTATTTCTGATTGAACTCTGTAACCTCAGCAAGTTTCAT
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAAAA
 AA
 AAG

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVYGTDVYASYSSVCGAHVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWR
ESFIVLESKPKKGVTPSALTYSSSKSPAQAQAGETTKAYQRPPIPGTTAQPVITLMQLLAVTVAVA
TPTTLPRPSPSAASTTIPRPQSVGHRSEQMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP
VGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPATFNLKTHTNRDLDKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTLLQPLVKRVCDDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISDTRIGAVQYTYEQRLFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAWAAQEELEVIATHPARHDSFF
VDEFDNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

[illegible][illegible]

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLLSLFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLTCLKTMAFRWVTEFCPNAKYVMKTDVDFINTGNLVKYL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGAGTTGGGGCTCACTTTTCTCAGCTCCTTCTCATC
TCGTCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCCGGAGCAGAGTGGAAATATCATGTGTCGGGAGTGCTGTG
AATATGATCAGATTGAGTGCCTCTGCCCCGGAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAAATGGCTCATGGGGGGT
ACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG
GCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCCATAATGCTCACTGTGAATGGACCATTTCATGC
TAAACCTGGGTTTGTCTCACTAAGATTTGTGATGTTGAGTCTGGAGTTTACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG
GATCCTCACTCCAGCTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC
ATGCTCCTCATCCCTTGTCTCCATGACGGCACGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTGGCAGGC
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACAGAAAA
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAATTTGGCACCGTGGTGTCTTTCTTTTGAACACTCCTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAAGCCTGCCGA
GAACCAAGATTTTCAAGCTGGTGAAGGAGAGTCTTCCGATGCAGGTTTCAGTCAAGGGAGACACCATTACACAGCTAT
ACTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGCCCCACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGG
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGA
CCCCAGGTTGCGCTGGCGGTGGCAGGCAGCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGC
GTGGTTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTTACCGGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCTTGCATCCCAACTATGACCCCATCTGCTTGATGCTGACATCGCCATCCTGAAGCT
CCTAGACAAGGCCGATATCAGCACCAGGAGTCCAGCCCATCTGCTCGCTGCCAGTCGGGATCTCAGCACTTCCCTCCAGGAG
TCCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCCAAGTGAAGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTTCCCGGGA
CGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTACCAAGGTGCTGCTCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACCTCCTTGAGAAG
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTTGGCCTGTGAACCTTGGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGTTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGCTTGCAAGAAGTAAGTTCTTCAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGTCTTCCCAACTTTTCAATTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCTTTGGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTT
TGTGTACATGGCCACAGTACAGTCTGCTCCTTTCTTCCCATCTCTTGTACACATTTTATAAAATAAGGGTTGGCTTCT
GAAC TACAAA
AAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII
KRVCGNERPAPIQSIGSSILHVLFSHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFQKQKLSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGIENITAP
KTQGLRWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC
TGAAGGTTCTCAGTCAAATTCCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGCGCTTCTGTTCG
TGGTCTTGCCTTGGCTCAGTCTGCTAACTACATTGACAAATGTGGGCAACCTGCACCTTCTGTATTGAGAACTCTGTA
AAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAATGGCTGTCCAGACGGCTGTGCGAGCC
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCTTGGCCCTAGACA
ACCCTGCCTACGTGTCTCGGAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACTCTGGCCGGAGCAACCGAATA
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA
GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGGAAAATTCTGAAAACACCACTGCCCTGAAG
TCTTTCCAAAGTTGTACCACCTGATTCCAGATGGTGAATTAACAGCATCAAGATCAATCGAGTAGATCCCAGTGAAA
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTATCGTGATGGGG
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
ACAACTACGCTGTGCGTCTCCTCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCA
GCAGGAACAATGGACAGGCCCGGATGCCACAGCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGAATAAACTGGTGCAGAGGTGGATGAGCTGGGGTTTTTCATCTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCAGAAAGTGCGGCTCATCTGATTAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCCCGCAGGTTCCGGCAGC
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACA
CTCCCAAGCCCTCCATCTACAACTACTTGTCTAGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCTCATGTTGAGCCCGGAGGAG
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTCAGCC
GGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT
GGGTCATGTGGCTGGAATTACCACGGTGCTTGTATACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGTCTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
TTTTATAGAATCAATGATGGGTGAGAGGAAACAGAAAATCACAATAGGCTAAGAAGTTGAAACACTATATTTATC
TTGTGAGTTTTATATTTAAAGAAAGAAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAATATGATTCAAAAAATTAATACTACTAGTTTTTTTTTTCAGTGTGGAGGATTCTCATTACTCTAC
AACATTGTTTATATTTTTCTATTCAATAAAAAGCCCTAAACAACATAAATGATTGATTGTATACCCCACTGAATT
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT
AAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAACAGAATAAATATTTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
PEVSAAATISLMTDEPLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFI FNVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQRSPDIFQEAGWNSNGSWSPG
PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPITYVISVEPGGVISRDGR
IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
SDWSPSWVMWLELPRCLYNCKDIVLRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
TTCCACCTTTCCCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
CACCAGTAACCTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAGCAAAGGAGTTCATGGCTAATTTCC
ATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
GACAACTGTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
CTTTACAGAGGGTGCCTCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACTACTGGGGAT
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCAATGACCC
TGATCTTTTGGTGATGTTTGAAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTCT
TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
CATGAGGGTTAAATATTGTAATATGGTACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
AGGTACGAAGATACAATACTGTTATTATTATCTGTACAATCATCTGTGAAGTGGTGGTGTCAGGT
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTGGGAATGAAGA
GGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLTFFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWWGGED
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG
CCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCACAACAG
ACGGGACAACCTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCTCCC
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTTGTTT
TCCAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 44

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATG
GTCCTCCTGTGTCTCCTGTTGGTGGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENTHEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTTCATCCAGAATCCTTCAA
CTTGCAAGTGGTTTTTCAATGACTCTTGTCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCT
CAGTCAGATAGTCATCGGTTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNPSNSNANCEFSL
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA
CATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT
TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS
SQKQHSPVPEKAIPLITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAGCTGGCTCTAAAGTCAGTGAG
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA
TTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG
GTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAG
AGCCAGCAACCAGAATGAAGGTTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGCGGAGGAAATGGA
CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGGAGCGGGGAATCTGGGATTACAGGG
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCAGCTCCCTCCTTAA
AACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAATAAACCTTAGCTGCCCCACAAA
AA
AA

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Signal peptide:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Cell attachment sequence.

APP ID=10063592

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTGCCGCCGGCTCCAGTGTTC
CACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGGCCAGTGAATATATTGCCACCAT
CTTGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC
GCTGTATCCGGGAGCGCGTCGCACCTCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGAGGCCATGACACCAG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGGCAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTCCGCA
GGGCCCAGGAACTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCCTGCCAGACCACTGAGCCCCGAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGCACTGACTTTCTGAC
CCATCCACCTGTTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWGHLG
LITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGEGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTTGGCGTGTGCTTGC
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGACGCAATGTGTTGCTT
GTGATTGGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA
GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGAATCTTCCTCATGTACCTGTTTCCTC
TCTGGATGTTGTCCCACTGAATCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA
AA

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCAGCCAGCAGGCCGCCAACATGCTCTGTCTGTGCCTG
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC
ATTTTCAAGCTCAGTGTCTTCATCCCTCCAGGAATTCACACCTACCGCCAGTGGAGCAGAAAATGTACAAGCT
GGAGATAAGGACCTTGATGGGCGAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG
CTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTACGCGCAGGAGATCATGCAGTCCCTGCGGGACTTG
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAATTCAGAGCATGGATAAAAAACGGCAGCATGACCATCGACTGG
AACGAGTGGAGAGACTACCACCTCTCCACCCCGTGGAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCCACG
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA
CACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG
CAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTGAGAAGGAGGGGCCAGG
TCACTCTGGCGGGGCAATGGCATCAACGTCTCAAAATTGCCCGGAATCAGCCATCAAATTCATGGCCTATGAGCAG
ATCAAGCGCCTTGTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCAGGGGCC
ATCGCCAGAGCAGCATCTACCAATGGAGGTCTGAAGACCCGGATGGCGCTGCGGAAGACAGGGCCAGTACTCAGGA
ATGCTGGACTGCCCGCAGGAGGATCTGGCCAGAGAGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTG
GGCATCATCCCTATGCCGGCATCGACCTTGAGTCTACGAGACGCTCAAGAATGCCTGGCTGCAGCACTATGCAGTG
AACAGCGCGGACCCCGCGTGTGTGTCTCTGGCTGTGGCACCATTGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC
CCCCTGCCCTAGTCAGGACCCGATGCAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC
TTCAAACATATCTGCCGACCGAGGGGGCCTTCGGGCTGTACAGGGGGCTGGCCCCCACTTCATGAAGGTCTATCCCA
GCTGTGAGCATCAGTACGTGGTCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTCCGGTGGCAGGGGGAGGGC
CGCCCGGAGTGGACTCGCTGATCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACACT
AAGCTGTCTCGAGCCAGCTGTGAAAACCTTAGACGCACCCGAGGGAGGGTGGGGAGAGCTGGCAGGCCCAAGGGCT
GTCTGTGACCCAGCAGACCTCTGTGGTTCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCAAGCAGG
CTCCGGGCTCACATGTGTAAGGACAGGACATTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGGCCGGCT
TAGTCTCTCCATTTACCCCTTGACGCCAGCTGTGGCCACGGCCCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGC
CCTCTGTGCTGCCCTGCTGTCTGTGAGGTAAAGTGGGAGGAGGGCTACAGCCACATCCACCCCCCTCGTCCAATCCC
ATAATCCATGATGAAAGGTGAGGTCACTGGCCTCCAGGCCTGACTTCCCAACCTACAGCATTGACGCCAATTTGGC
TGTGAAGGAAGAGGAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGCATG
CTTGGGAGTGCAGGGGGCTCGGGCTGCTGGCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT
GGCCTGGACCTGTGAGGATGGGGCCACCTCAGAACCAACTCACTGTCCCACTGTGGCATGAGGGCAGTGGAGCA
CCATGTTTGGGGCGAAGGGCAGAGCCTTTGTGTCTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCCTTAATTATGG
ACTGTTGGGAAAAGGGTTTTGTCCAGAAGGACAAGCCGGACAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTCTCTGTCCAACCCAGCAGGGGCGCAGC
GGGACAGCCCCACATTCACCTTGTGTCACTGCTTGGAACTATTTATTTTGTATTTTGAACAGAGTTATGTCCT
AACTATTTTATAGATTTGTTAATTAATAGCTTGTCACTTTCAAGTTCACTTTTATTCATATTTATGTTTATGTT
GATTGTACCTTCCCAAGCCCCCAGTGGGATGGGAGGAGGAGGAGAGGGGGGGCTTGGGGCGCTGCAGTCACATCT
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGGCAGCAGCCCTGGCTCCTTTTCCCTTGGCAG
GTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGGGCTGGAGAGAGGGGAGGAACCTCAAT
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG
TGAGGTGCTCTCACTGTGAATTTGTGGTGGGCGGGGGCTGGAGGAGGGTGGGGGGCTGGCTCCCTCCCTCCAGC
CTTCTGCTGCCCTTGCTTAACAATGCCGGCAACTGGCGACCTCACGGTTGCACTTCCATTCCACCAGAATGACCTGA
TGAGGAATCTTCAATAGGATGCAAGATCAATGCAAAAATTTGTATATATGAACATATAACTGGAGTCGTCAAAAAG
CAAAATTAAGAAAGAAATGGACGTTAGAAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTCAAAGCTGAAAAAA
AA

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSI FKL SVFIP SQEFSTYRQWKQKIVQAGDKDL DG
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMWWRHLVAGGG
AGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESA IK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAI AQSSIYPMEVLKTRMALRKTGQYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVRTRMQA QASIEGAPEVTMSSLFKHILRTEGA FGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTGAACCTGACATCAAACCTTTCTGATAT
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
AGCTGTGCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGCTGATCAAGTGATAGTT
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATAC
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
TCAACAACACATACTCCTGTATGATTGAAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
CTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAAT
GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGA
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
TGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
GCTGCATTTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6o

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYIMLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATTGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
GGGCTACCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG
GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCAGCAGCCT
GGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGAAGAACCCTCTT
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
TCCTGGCTTCTTAGAGTGAAGAGATATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAAATGG
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGATTCTGCCACACCCATAAAT
CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTGCAATTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH
SGYISMKELKQALVNCNWSSFNDETC LMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSOMGYNLSPOFTQLLVSRYP R SANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDEFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC
AACTTGCCCTCAGCTCGGACAACCTTCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCCG
TCTGGACCCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCTGGGGGA
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCTTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTTCCTGCCTGATCACCCCTGGGGTACCCTGAATCCCACTG
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGCTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCTGCTCCCGCCCCTTGCTG
TGTGGGCTCAATCCAGGCCCTGTAAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPFAGGSAVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRRLPRNSLGAGGKILSQRP
PWSLIHRVLPDHPWGTINPSVSWGGGGPGTGWGTRMPHPHEGIWGINNQPPGTSWGNNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCTTCTTGCCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MGSGPLVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCTGCTGGCCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCTGCCCCATCTAGGTCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTGTGTTTCTCTTAGTTCTGTGCTGCTGCACCAG
TCAAATACTTCTTTCATTAAAGCTGAATAATAATGGCTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
GATGAAAAAATAATGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
TTTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAACATGAA
AACATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCATACACCAAGCAGTTCCACA
GAATGTGGAGAGAAAGGCCGAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAAACAATAATGAATATGGACCA
CCAGGCCAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCCTTTC
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT
CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACACAAAACGTATGGAAAAAGATTGTCAATTCTTT
CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGAACGAA
AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGAATTTTGAAGTACATGGGAGGTGATTAGCAAT
TCTGAGGATTTTAAAAACACCATACCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTTGCTGAAGATCAGTCAA
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAGGACCGCTAAATCGAATGAATCAAGCAGCA
AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA
AATAAGCTAATCCAAATAAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA
ACTTCCATCTGCTCTGGAATTAATATGCATTTTCAGGTGATTGGAGAGCTACATTTCCCAACTCGATGGATCCGAAGTA
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTGAACAAAAGTGGGGCCATTGTTTCTAT
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT
TCAGATGAAGCTCAGAACATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAG
TCCCTTCAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCATAATTGATAGTACA
GTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCGAGTGGAAACA
ATAATGAAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACTGCAAGGTGGGCACT
TGGGCATACATCTTCAAGCCAAAGCGAACCCAGAAACATTAATATTACAGTAACCTCTCGAGCAGCAAAATCTTCT
GTGCTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCAATGATTGTTTACGCAGAA
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCATGTGACTGCTTTTATTGAATCACAGAATGGACATACAGAAGTT
TTGGAACTTTTGGATAATGGTGAGGCGCTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT
ACAGAAAATGGCAGATATAGCTTAAAGTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCCTCCA
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATGGAAGCAAAACCCGCAAGACCTGAAATTGAT
GAGGATACTCAGACCCTTGGAGGATTTTCAGCCGAACAGCATCCGAGGTGCATTTGTGGTATCACAACTCCCAAGC
CTTCCCTTGCCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTTCATGAGGATAAGATTATCTT
ACATGGACAGCACCAGGAGATAATTTTGTGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATCTT
GATCTAAGAGACAGTTTGTGATGCTCTTCAAGTAAATACTACTGATCTGTCCACCAAGGAGGCCAACTCCAAGGAA
AGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCCACATATTTATTGCCATTAAGATATAGATAAA
AGCAATTTGACATCAAAGTATCCAACATTGCACAAGTAACTTTGTTTATCCCTCAAGCAAACTCCTGATGACATTGAT
CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTATTG
TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTTC
AAGTAGACCTAGAAGAGGTTTTAAAAAACAAAACATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT
GTGTGATCATAAACTCATAAAAATAATTTAAGATGTGGAAGGAGGATACTTTGATTAAATAAAAACACTCATGGATA
TGTA AAAA ACTGTCAAGATTAATAATTAATAGTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAACAAAG
ATCCTTTTTCTACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTTCTGAAATGATATTTCAAATTCATCAA
GAAATTAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAAAATAAACACATTTGGAAAAA AAAAAA
AA

FIGURE 70

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFE
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLLLGLKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVEFCNEKTHNQEAP
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR
MNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPITYPLGGTSICSGIK
YAFQVIGELHSQLDGSEVLLLTGDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNDGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRLPPLNRAAYIPGWVVNGEIEANPP
RPEIDEDTQTTLEDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDN
FDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI
VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGAAAGACCATACGTCCCGGGCAGGGGTGA
CAACAGGTGTATCTTTTGTCTCGTGTGTGGCTGCCTTCCTATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGCGTTGGAGGAGAGAACCTTTGCGGGCTCGCTTCTCTTAGCA
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCCCTCTGCTGTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCTTTAAA
AGTAGAGAAGCTGCTCTGTGTGGTGGTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAAGGAAGCCCTTCCGTGGGGGGCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCTGAAATGATGATGGTTCGCGGGGGGCTGCTTGCCTGGATTTCCCGGGTGGTG
GTTTTGCTGGTGCCTCTGCTGTGCTATCTCTGCTGTACATGTTGGCTGCACCCCAAAGGTGACGAGGAGCAG
CTGGCACTGCCAGGGCCCAACAGCCCAAGGGGAGGAGGTACAGGCCCTCTTCAGGAGTGGGAGGAGCAGCAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG
AATGGGCGAGTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC
CTGGCCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGGCAGCTG
CCTTTGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTG
AGGAAGGACAAAGCGGATGAGTTGGTGAAGCCATTGAATCAGCCTTGGAGACCTGAACATCTGCAAGAGAACAGC
CCCAATCACCCTCCTTACAGGCCCTCTGATTTATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGACATTGTAT
GAGCTCAACCTTCAAAGGGGACACAAACACGAATTCAAACGGCTCATCTTATTTGACCACTCAGCCCCATCATGAAA
GTGAAAATGAAAAGCTCAACATGGCCAAACAGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAGTTC
CGGCAGTTTATGCAAGATTTAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAAGAAATAAATGAAGTCAAAGGAATCTTGAAAACACTTCCAAGCTGCCAAGCTCAGGAACTTTACCTTCATC
CAGCTGAATGGAGAATTTTCTCGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGAAGCAACGCTCTTCTC
TTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAG
GTATTTTATCCAGTTCTTTTCACTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA
CAGCAGCTGGTCATAAAGAGGAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTGAGTATCGGTGAGAC
TTTATCAATATAGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGAGCAGTACAAGATGTGCATGCGAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGATGGTG
GTGTTCAAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGACAAGTAGCAAAAAACATGAAGTCCCAGA
GAAGGATTGTGGGAGACACTTTTCTTCTTTTGAATTAAGTGAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA
GGACGCAAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAACAGA
AATCAAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTGTACAAATACACTGAGACCTGTTGTTTGTGTGCTCATTGA
AATATTTCATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTCTCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGATAGGCTTATTATGATACT
AGTGAGTACATTAAGTAAATATAATGGACCAGAAAAGAAAAGAAACATAAATATCGTGTATATTTTCCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTGGTTGTCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACT
TTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTAC
ATTTTATATTTTTTAAGAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTGATGCCATAT
CCAAGGCATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCACTTGAACATAGGGAAGGAATGGTTGTACT
AATACAGAGCTACAGATACTTCTCTGAAGAGTATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAGAAAATGAC
ACTTTCTGCTTTACAGAAAAGGAAACTCATTGAGACTGGTGATATCGTGATGACCTAAAAGTCAGAAAACCAATTTT
CTCCTCAGAAGTAGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACCAATCTCTTTTC
AAAAAGGGTGTCTCCTGCTGCTTCTGGCTTCCATAAGAAAGAAATGGAGAAAAATATATATATATATATATATTGT
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACTGAATTATTTTTAAATTAAGCAGTTCTACTCAATCACAAGATGCTTCTGAAAATGCAATTTATTACCAATTT
CAAATATTTTTTAAAAATAAATACAGTTAACATAGAGTGGTTTCTTCACTCATGTGAAAATATTAGCCAGCACCAG
ATGCATGAGCTAATATCTCTTTGAGTCTTGTCTTCTGTTGCTCACAGTAACTCATTTGTTAAAGCTTCAAGAAC
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGATTGATTGTACTGGTAGTTTATGAAATTTAATTTAAACACAGG
CCATGAATGGAAGGTGATTGCACAGCTAATAAATATGATTGTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQV
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLN
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFR
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPV
LFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGG
EDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDLTPEQYKMCMSKAMNEASHGQLGML
VFRHEIEAHLRKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

[illegible][illegible]

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEAT
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGTGTC
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTACTGCGTACACGTGGAGTCTTTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCATATCTATTACCGTGTTCCTTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCTGCTGAAAAATCGTGATTA
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCAGCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTGAGAACCCTGACATTTGTGCGGGGCCGTAAGAGCAGGA
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCGCAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCTGGTCTGACTGGGA
TCCCCAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTTATA
TGTGCAGATGGAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTAGTGT
CTGTGAGAATTACTTATTTCTTTTCTTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQOIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYGNEDKRFFVPAEK
IVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQ
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
CTGGGAAGATGCGCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
CAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC
ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA
TCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
CCCACCCGCCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTA
TAAGCTCTCCTTCCCTGGTGAACGCCTTAGCTAAGCAGGTTCATGAACCTCCTAGTGCCATCCCTGC
CCAATCTAGTGAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGACTCACAGGGAA
AGGTGACCAAGTGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCCTGTTGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGTGGAAGTGTT
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG
CCTTGGGATTTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACTTG
CCTGTGAAAAA

FIGURE 78

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAMREK
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLDFDLLYPAIKGDTIQLYLGAKLLDSQGKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG
FEAAESSLTKDALVLT PASLWKPS SPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGCCCTCCAACCTTGTTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAGGCCTCCTGGGATTC
ATTCTGTGCTGCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCC
TCACCTTGCTGCTCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVG YILG LLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTT
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCTGCCCCTCCTTTCTT
GCCCCCGCTGCTTCTGCCCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
GTTGATCTGTGGCCCCGTGTCCTCCGTGTCTTTTCGTCTCCCTTCTCCCGACTCCGCTCCCGG
ACCAGCGGCCTGACCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA
CTCGCGTGTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
GTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAG
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCTGCCCAACCAGTGTGTCTCTGCAGCTGC
ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCC
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
AGAGGCCCGGGCACCCACGCCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT
GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGG
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTC
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
CTCGGACTTGGTGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAGGAAGTCACT
GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGACAAAGTGACCAAG
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNMTMYQHGEIFSAHELF
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPPTAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKHKACVHGGKTYS
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPKVAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCATCCGTCACCTCTCCTGTCA
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAAGTGGTGAAGGATTCTATTGCGGAGGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTGAGTCTCGGCTGGTTCCCCCGGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTTGTCC
ACAGACTCCAGGACAAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCCGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
GAGATACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATCCAGTGGAAAATCCAGGCGGAAGTGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGTAAACCATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT
ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTA
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGTTTG
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAATCCCATAGTCATCTGC
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG
TGAGTCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGTCTCTCACTCCATCTGGCTAAGTGTCTTGAATACCACTCTCAGGTGAAG
AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSQWQVFGPKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTDSTRNDRMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAE LDWRRKHGQAE LR DARK HAVE VTLD PETAH PKLCVSDLKTVTHR KAPQEVPHSEKRF
TRKSVVASQS FQAGKH YWEVDGGHNKRWRVGVC RDDVD RRKEYVTLS PDHGYV LRLNGEHL YFT
LNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAI PETSNSSESSQATT PFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCCCCCT
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
TACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCC
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCCCGCTCCTCGGTGCTCACCCCTCATCCACA
GCCCCAGGACCATGGCACCAGCCTCACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCT
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA
GAGGCCGTGACCCTGTGCCCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCT
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGA CTGAGGGGTGGTGGGGGAGCTGGAG
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTT
AGCCTCTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG
CTTCTGCCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCCCTCCAGGCAAGGGAGAAGTCA
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC
TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPPMISWIGTSVSPDPSTTRS
SVLTLIPQPQDHGTSLTQCQVTFPGASVTTNKTVHLNVSYPQNLMTVFQGDGTSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGTGIE
DANAVRGSASQGPLEPWAEDSPPDQPPASARSSVGEGLQYASLSFQMVKPWDSEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVIPIVVYDFGDAQKTASYYSPTYGQREFTAGFVQFRVFNNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAAC TTCCAGCCTCAGAGAC
CGCCGCCCTTG TCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTTCGTACACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATT CAGCTGGTGGCCGCGCTCT
CTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC
AGCAGCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT
ATTCGAGCGTTGGGAGTGCAC TACGTATTGGTACATTTTGTCTTCTGCAGTGCCCTTCCAGCTG
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTTGGGAAGAAGGAAG
GCATAGGCTTCGGTTTTTCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA
TTAAGACTTATATACAGTTT TAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQIDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCTCCCGGCTCAGAGGACCTTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC
CACCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGGCCCCAGTAAAGCTGTAG
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACATC
CATAGTGATACCCCTTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGGCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGTGTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACGGGGTTCTCCCGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCGGGCCGAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFAQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTAT
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVSGLGFGIMSGV
FSFVNTLSDSLGPSTVGIVHGDSPPQFFLYSAFMTLVIIILLHVFWGIVFFDGCCKKKGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKCLLCQDKNFLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAACA
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC
CAATTTTGTGCACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
GAACCCAGCAGGCCGCCCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
TACCTGAAAATATTCTTGAAATTTAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAACATATTTGGAAAACCTGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGACCATG
GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCAAGGCCAGCCTGC
AGAGCTGTCTGTGGAAGTTCCAGAAACTATGGTGGAATTTCCCTTTATACCTGACCAAGTTGC
CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGTGGTGACAGGGCCCTGGACCGAGAGGA
GCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC
AGAGCTCGGCTGAGCCGGGGTACCAGGCCCTGGCATCCCCCTCTCTTCTTCTGAGGCTTCAGACCG
GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCAGC
CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
CCAGGCCTCAGGCCACCCAGGCACTGCCACCGTGGAACTCTCCATCATAGAGAGCAGCTGGGTGT
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTATACCCGACCCACATGGCCAGGTA
CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTTGAAGTGAA
TGCAGAGGGAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC
AGGTGCGGGCTCAGAATTCCTATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG
ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
CAGTCCACCAGGTACTGAAGTGACTAGACTGTGACAGAGGATGCAGATGCCCCGGCTCCCCCA
ATTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
CCTGCTTCTGGTGTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
TCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGATTGGGCCT
ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
CCTCGAGCCCGCCTTCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCC
AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCCCAAGTTGG
ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTCTCTGCTGACCATC
CAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
CTGCATTGAGAAATTTCCGGGGAGGTGCACACCGCCCACTCCCTGCAGGGCGCCAGCCTGGGG
ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT
GGCCAGTGGGCACGGTCCCTACAGCTTCACCCCTGGTCCCAACCCACGGTGCAACGGGATTGGC
GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGT
GAACACATAATCCCGTGGTGGTGCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTGAGTGAT
CGTGTGTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA
CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCTCATCCTC
ATTTTACCCACTGGACCATGTCAAGGAAGAAGACCCGGATCAACCAGCAGACAGCGTGGCCCT
GAAGGCGACTGTCTGAATGGCCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
TCCCCTGGGAGAGAGCCAGCACCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA
TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCACTT
TATGGACTGCCCATGGGAGTGTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCAGAGAA
CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSPQALPKAQPAELSVVPEVNYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLVTRALDREEQAEYQLQVTLEMQDGHVWGPQPVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADADLEPAFRMLDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY
EAAPSHEVWVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTILAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGNPTVQRDWRLQTLNGSHAYLTALHWHVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTLLVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGCCCTG
 AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
 TCTCTTACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC
 ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
 TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC
 TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
 TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
 GCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
 TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
 GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACT
 CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
 AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
 CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
 GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
 AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA
 GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
 TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
 GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGACAGCCACCAACT
 CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCAGTCCAGTCCAGTCCAGCACACCCTCC
 AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC
 CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGTCCAGACA
 GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
 CACAGTGTCCAGTGGGATCAGCACAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG
 ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
 ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGTGAGGCAAGCCTGGTGGGTCCCTGGT
 GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
 TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCCT
 CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
 GTGGAGTCTTAAGTGTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
 ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
 CCAAGACCTGGTTTCTTTTCTTTCATTCATCCCAGGAGACCCCTCCAGCTTTGTTTGTGATCTGAA
 AATCTTGAAGAAGGTATTCCTCACCTTTCTTGCTTTACCAGACACTGGAAAGAGAATACTATAT
 TGCTCATTTAGCTAAGAAATAAATACATCTCATTAACACACAGACAAAGAGAAGCTGTGCTTG
 CCCCAGGGTGGGTATCTAGCTCTGAGATGAATCAGTTATAGGAGAAAACCTCCATGCTGGACTC
 CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MRMQKGNVLLMFGLLLHLEATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNESSTTSSGASTATNESSTPSS
GASTVTNSGSSVTSSGASTATNESSTVSSRASTATNESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNESSTVSSRASTATNESSTTSSGASTATNSESRTTNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNESSTTSSGASTATNESSTTSSGASTATNSDSSTTSS
GAGTATNESSTVSSGISTVTNSESSTPSSGANTATNESSTTSSGANTATNESSTVSSGASTA
TNSESSTTSSGVSTATNESSTTSSGASTATNSDSSTTSEASTATNESSTVSSGISTVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRRWSPNWFWRPVSSI
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG
GGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCAATCCAGGGGAAGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTGTCATGGAAGGGATTTACTTTATACTGACTCTGTTTTGGGGAAGCTTTTTGGAAGCATTT
TCATGCTGAGTCCCTTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGGT
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTCATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGTTGGTGGCCATGCAGGCTGCTGCCTATAT
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTGGAAGACATGATTGATTACTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCCTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACACATTCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTTACGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCATTCCACCTGCAAGTCTGAACTCAGGGTC
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTAAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTGTCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACT
GCCATCATTATTTGTTAAAGATATTTTCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTTAAA

FIGURE 102

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIFMLSP
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
FLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWDDKSHFEDMIDYFCDIHEP
LQLLIFPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLQGDFFPREIHVHRYPIDTLPTSKEQLWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPPCKSELRVLVVLLSILYWTLESPAMCLLIYLSLVKWFITITIVFVLQERIFGG
LEIIEIACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCTTTTGTGCTCATTGTTGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGTTTCTCAGGAATCAGTTCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGTTTCCCCAGCCACAGCCAAGTGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA
TTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAGGGGAAAATCCAGGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCG
TTTCTGATCTGAAACTGTAACCATAGAAAAGCTCCCCAGGAGGTGCCCTCACTCTGAGAAGAGA
TTTACAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACA
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT
ACATTCATCCCATTTTATCAGCCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCTGC
TGACATGTGAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTCTATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC
CCCACACCACAGACCCAGACACAGCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCCTCT
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTT
TGCTTATTCCACATTAATTTACTTTTCTCTATACCAATCACCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC
CTCATTAACACAGACACAAAATTTCTAAATAAAATTTTAACAAATTAACATAAACAATATATTTA
AAGATGATATATACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTAATATTTAAAT
ATCAACCAGTGTAATTCAGCACATTATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLVSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
TTTGTGGGAACCCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA
CTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC
TGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTCTACTCTACTGAGGATCCTGA
AACTGTAGATAAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
ATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
TTGTGAGTGTCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
ATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAATACAAACCCCATCACA
TGACTATGATATTCTCTTCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTGTC
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
GCCAGGTGACTCTGGAGGACCCTGGTTAGTTTCTAGATGCTAGAGATACTGGTACCTTGCTGGAATAGTG
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTGTTTACTAGAGTTACGGCCTTGCGGGACTG
GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTG
GGTGTGGAGGCCATTTTATAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
GATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
ATTACAGCCTGTATTCTATTTGTTCTCTAGAAGTTTTGTGAGAATTTTACTTGTGACATAAATTTGTAAT
GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTCAGCAAATATCCATTT
TCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAA
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTCTATTATGAAAGGTCAAGCAAAGACA
GCAGAATACCAATCACTTCATCTTAGGAAGTATGGGAAGTAAAGTAAAGGAGTCCAGAAAGAAGCCAAG
ATATATCCTTATTTTCAATTTCCAAACAACACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT
ATAATAATTATACAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGGAAGAAGTTCCCTG
CCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCCAGC
GCCGACGATCGCTGCCGTTTTTGCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
ACGGGGCTCACAAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA
TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTTCCT
GTGGTTCATCCGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTG
TGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTGCTTGTCAATTTTCT
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTTATGGTTCAGTACAATGGTCA
GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA
TGCTTGAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTCACTGACTGGTTGG
AAATGACAGAGATGGACTGGCCCCCAGATTCTGCTGTGTAGAGAATCCCAGGATGTTCCAAA
CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTTCCTT
TTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG
ACAGACCAATGATGTCTTGAAGAATGACAACCTCTCAGCACCTGTCATGTCCCTCAGTAGAACT
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAACTTGTTTTATTGGACT
TGTGAATTTTGTAGTACATACTATGTGTTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAA
TAACACCTAAGCATATACTATTCTATGCTTTTAAATGAGGATGGAAAAGTTTCATGTCTAAGTC
ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCGCA
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
CTCAGCGATCTATTCTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT
ACCTAAATGTGATTTTGTCTGGTTACTAAATATTTCTTACCCTTAAAAGAGCAAGCTAACACAT
TGTCTTAAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTGAGTCGAT
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT
ATTTTTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC
TGTTATTTAAATACTTAACCACTAATTTTGAAAATTACAGTGTGATACATAGGAATCATTATTC
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGA
AAGGACTTGTATGCTGTTTTCTCCCAAATGAAGACTCTTTTGCACATAAACACTTTTTAAAAA
GCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTCTACAGAAAA
TAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT
CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAA
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTATTAT
TTCTCAGAAATATGAAAGAAAATTAATGTGTCAATAAATATTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSLDLYQEGCGKMYSFRLGRTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCCCCTACCAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG
CCTCTTCATCACAGGCACCTCCGTGTACCCGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACCAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACCTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCCTGT
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCCTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCTGGTGTGT
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGTTTGGTGGCTGGAGCTCTTCTGACCAACACCTCTGCGGAGGAGTGTCCAACGGCACCCTATGTCAACAT
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCCAAGCAGACCCCGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG
ACCTGCGAGTTTCCACGCCTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT
CATGAGCCGAAATCATGGGATCTTCCCATTCACCTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCCACCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGGTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGCGAATGCGTCGTGGGGCAGGAGGAGAGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGGCGGCGCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACC GCCCTCTAAGAACATCTGCCAACAGC
TGGGTTACAGACTTCACACTGTGAGTTCAGACTCCAGCACCAACTCACTCTGATTCTGGTCCATTAGTGGGCA
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGTTTCATCTTTCTAGGGTTGAAAATAAATGTCCA
CCCAGAAAGACACTCACCCATTTCCTCATTTCTTCTTACACTTAAATACCTCGTGTATGGTGAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAATTAAACAGTTACTGAAATTATGA
CTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA
TTATAGGGAATTTGGAAGTGATCAATAAAACAGTATATAATTTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDQQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDICEDECHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSNHTCQVPVLCKSNAIEVNIIPRELVGG
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVDVVDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYILIRGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGGCHRRMRGAGGEDSAGLQGQTLTGGPIRIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC
ATGGAGACCTTCAGAAAGGTGGGGATCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
GGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCCA
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
AGGGAAGTGGTTCTCTGCCTGTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
GAGCTTCGCATGCGGAACTCAAGTGGGCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTG
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA
GCCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAG
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAGACAATGACA
TCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
GATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGT
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGT
GACAGTGGTGGGCCCCGTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
CTGCGGGGGCCCCGAGCACCCAGGAGTATACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTGCACTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
TTCTTGAGCAGCAAAGGGCCTCAATTCTGTGAAGAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCA
GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
CAGGGGTATTGCTAAGCCAAGAAGGAACTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC
CAGATCACTGTGGGCTGGAGAGGACAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
GCCTACTAGAGCAAGAAACAGTTGTAATATAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA
AAAA

FIGURE 112

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAEACRQMGYSRAVEIGPDQDLVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAHCFRKHTDVFNNWKVRAGSDKL
GSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSSGGPLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAATC
TGTTTTTTGTTCTCTTGTAAGTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGACAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTATAGGGGATGGCTCCCCTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTTCATGTCTGCACATCACCTG
ATCCATGGGCTAATCTGAACCTGTGTCCTCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCACTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTGAGAAAAGATG
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTT
CAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTGAATTTGAAACCCCAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA
TGTTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFGQGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGATTAAAGTGATTCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTCTTAAAAATTCCAAAATTCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGAGAAGATCTTCACTTTCTGCCAACGAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTG IYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCTCAGGAGCGGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGGCGGGCGGCCAGGATCATGTCACCACCACATGCCAAGTGGTGGCGTTCTCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCACATGCTGGTGACTAATTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTGGGCTGGGTGCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTGCTTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCAGCACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAAACAAGGAGATCCCATCTAGATTCTTCTTCTGCTTTTGACTCACAGCTGGAAGTTAGAAAAACCT
CGATTTCTATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTCAATCCTCTATTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCTCTCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAGAAACTTTTGAAAGGAAA
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTGAATTTTGTCTCCCCACCCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAGTCCCTTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA
TGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGGGAGTCC
AGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCCTAGAAAATCGCTGGGCTGTTTCTTG
GTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCCTCAGTGGAGAGTGTGGCCTTCATT
GAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
CATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG
GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
CATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATA
ACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA
CAGATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG
TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAAGCCATGCAAAATG
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT
AATCTTAATTACAGGAAGTGTGCATCAGCTATTATGATTCTATAAGCTATTTACGAGAATGAGATA
TTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
CTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
ACGACATAGCATTATGTACATAGATGAGTGTAACTTTATATCTCACATAGAGACATGCTTATATGGT
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAAATGTCCTCCA
TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTCTTCTCCAGAGGCTTTTTTTTT
CTTGTGATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTGCATTCAAACCTGCTT
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
AAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA
TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
GCTCCTATGTGGGTACCTGAGTCAAATGTCAATTTTTGTCTGTGAAAAATAAATTCCTTCTTGTA
CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAA
ACTGACAATCCAATTTGAAAGTTTGTGTGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
TATACATTTATATTAATAAATGTACATTTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMQWRVSAFIENNIVVFENFWGLWMNCVRQANIRMQCK
IYDSLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGGGCGGAG
CCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCCTCCAGCTCCGCGCTGCCCCGCGAGCC
GGGAGCCATGCGACCCAGGGCCCCGCCCTCCCCGCGAGCGGCTCCGCGGCCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCGCGCGCTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATG
GATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC
AAGCAGTGTTTATGAGATTGATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAAGTGGCTCACTTCGGCTAAAATGCA
GAAATGCATGCTGTCAGCGTTGGTATTTTACATTCAATGGAGCTGAATGTTTCAAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCAATTTGCTACCTCTTTTTTTATATGCC
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTCTTTCTCTTAGTATAGCATTTTTA
AAAAATATAAAAGCTACCAATCTTGTACAATTGTAAATGTTAAGAATTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAAGVPGR
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTINIHRTS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
CTGGGTGCTCATCACGGGAAGTGTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
ACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
TCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTCTATGCAACTG
GCCCCAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCCACTGTCTTACTGACAATG
CTTTCTTCTGCGGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGA
GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATT
TACGGAACCTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA
AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
CTGGCCCTTTTTCCAAGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGT
CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
TCGAAGCTTTTCACTGGACCCAGTGTTCCTCAGTGTGTCCCGAATCTGCAGCGCTCAACCTGGAT
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGATTCTTGATATCCCTCAATGACATCAG
TCTTGTCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTGAAAAGTT
TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG
GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAAACCCCTT
TGCCCCGACGGTGGGAGCCACAGAGCCCGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT
CTACGTGTCTATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTA
GATTATAAACCCACCAACACGGAGACAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTATAAAAAGAGCTCTTAAAGCT
GGGAAATAAGTGGTGCTTTTATTGAACCTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTATAATACT
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
GAACTCCGGTTTAAATATAATACCTATTGTATAAGACCCTTACTGATTCCATTAATGTCGCATTT
GTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLKSLHLSNSLRITIPVRIFQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLQYQWNKISVIGQTMSTWSSLRDL
SGNEIEAFSGPSVFCVPLNQLRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSEFKGLRENTIICAPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCTGGATCTCACAAAACCTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG
ATGAGCATTATCCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
TTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAGATGCAAAATGGAAGGAAAAAGGAACTGGAAGG
AAAACCATTGCGATTTCTGTTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACCTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACC
ATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES
APYRCMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRLKLGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTPVKHYLVNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGGCAGGAGAGCGGGCGGGCGTCAGCTCCTCGAC
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCGCTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACTTTGATCCCCTACAGATGTGACCTAT
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCGGCGTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAAATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCCGTGCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT
CACGGGATACCACCTTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTCTTGTGCCCTGGGCACCTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCCAGTCTTGGCTTCTTGTCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCAGTGGATTTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAA
AAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVGCAITVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDITLLSGSTSGWKDMFNVLALSICTR
EAYQSMKERNVDDGHIININMSGHRVLPVTHFYATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCCCTCCTTTGACTGCGGGCCGTTCAAGTGCAGAGTCTCAGTTGCCCCGGAGC
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCTGTTCTGTGTCTGCGCTGTTTCATTTCACTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAATGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTTCTCATTTATTTA
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTGCCTCGGCCTCCCAAAGTGTTATGATTACA
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGGAACCTTGAAATTAT
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAAATGACAGGATTTCTGTTCTTAATTTCAATTAAATAAACCACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFCRVSVAREHLPSRGSLLRGPRPRI PVLVSCQPV
KGHGTLGESPMFPKRVFQCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTCAGAT
TTGAAAAACTTGCTGAAAGTAGAAAGAATATACCTATAACCACAACAGTTTAGATGAATTTCCCTACCAACCT
CCCAAAGTATGTAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCCGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTTT
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG
GTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAACCTGTTGAAACAATCATGGTTTAGGTGACAAAGTT
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCAGAAATCCCTGACTGCTGCACCAGTAAACCT
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATGCGGGTGCAAGATGAAATG
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
AGGTTCTGGGGATGGCTATTAAGGATCTCAATGCAGAAGTGTGATTGTAAGGACAGTGGGATTGTAAGC
ACCATTCAAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCAATCTCTTGGAACTTGCTCTACCTATG
ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTGGATCTATAACAGAAACAATTGT
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCTATAAAGTATGCATGGTTC
CCATGGAAACCAGCAACCTCTACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTT
CGAATGTACAACCCCTACAACCACCCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC
TTTGGCTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATGCCCCTCTTGCTTTAGTGTGTTGGTATG
TTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTTCTTTTCAGATGTTACCAAT
AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCATATTTCCCTAATGGAATGAATCTGT
ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL
EELHLLDDNSVSAVSIIEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLNDITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTQKPD
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSPYKVCMPMETSNLVLFDETPVCIETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIALLLVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSNRSYRDSGIPDSDHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCCAGGCTTCTTGCCA
GCCCTGCCGGGCCACTTGTCTTCATGCTCTGCCAGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCCTGTGGT
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
GCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
GGGGTCCGAGTGTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCAGGAGCCCCTGC
TGCAGCCGCTGAGCCTGCGCGTGGGGATGTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCGG
GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGGC
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
GACAGCAGCGAGCCCTGCGGCCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
AGGCTACTGCCTGTCCCACCAACTGCTCTTCTCCTCTGGGCCAGAATGAGGGGATGCACACAGG
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
AGAGCTGAGGCCATCGGATACGCCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCCTCCTGGGTTCAAGC
AATTCTCTTGCTCATCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT
TTTTATATTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG
GTGGCTTCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAA

FIGURE 134

MSARGRWEGGRRACRGSGLARAQGAERVTSSQRPAMASLGLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLIISALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQTLQPGFWKLPHAWIHTDASLVYPTFGPDSEFSEE
RSDVCLVQLLGTGTDSSPEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSQKQEGCFG
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCA GTTGTTCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCCGAGTGTGGTAGACGGAGAAGAGCACGTGCGTTTCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCCAATGGT
TATGATGATGGTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT
AACTTTTGTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSAPYRFDPPVRVDITSKGKMRARYVNYIKTSE
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME
QSMNMLNSNHELDPVSEFMTRLFSSKSSGSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAA
GTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCCTGCGAATCGATGCTGCGCTCCTGCGCCATTGCTAAGACTCTATCTGGACAGGGTATTTAA
AACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
CTTCCTTGCAATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA
ATGTATTTATTTTTTTACTTGGACATGAACTTTAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAATAACCTTGTAATTTCTAGAAGAGTGG
CTAGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCATAATTGTGTATCTTCCAG
CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAA
AAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATT CATNSHSDSELRPEIF
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLTIKKDLRLSHAMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC
 TAGCGTGTCCACGATGCGGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
 TAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCCAGAGCGGAA
 CACGGAGCGGAGCCCCAGCGCCCCGAACCCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
 ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTG
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGAAAAAGGAGCATCTCACAGT
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
 CCTTCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA
 TAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA
 TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGT
 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCC
 TCCACTACCTGGGGCTGGACCACATTTGGCCACATTTAGGGGCCAACAGCCCCCTGATTGGGCAG
 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTGAAGGAGAGAGA
 GACGCCCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG
 GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAGGAAA
 CCCGGTGATATCCGACATCCAAAGCAGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC
 ACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGAAGGAAGAC
 CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG
 AATGTCCGTCATATGAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGG
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTCAGAAGTCTATTCAACCTGGGCTCCAAGG
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG
 TTCTCACCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA
 CTGTCTCTCCTGGGTTTCTCTGCTCTTTTATTGTTGATCCTGGTTCTTTCGGCCGTTACAGT
 CATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT
 GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCCTGGAC
 AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCCTGCGGTGTCCGACACAGGTG
 TTCACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAAGCTAGGTTCTGCGACTGTTAC
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
 TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
 CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCTGCCACCCCAGAATGCATCCT
 GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTCTGTTGGAATCTTAGTCCCTGGCC
 TCGGACACCTTCATTTCGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
 ACTCAGATCCACAGAGCCCAGGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
 ACCCAACCCTGCACAGCCCTCATCCCCTCTTGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGT
 CTGACCGAGACACTCACAGCTTTGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTG
 CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG
 CTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDSDVIRQAKAAGKRIVFYGDETWVKLFPHFVEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDHLHIGHISGPNPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCTTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC
TCCCTATAGAAAACAACCTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTGAGCATTGATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAACCTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCT
GGCTGCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTGAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAACACCAAACCTGCTCACT

FIGURE 142

MLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQHKVLVLDSGNLIAVPDKNYIRPEI
FFALASSLSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI
FYRAQVGSWNMLESAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCCTTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCTGGGCGCTGTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGTCTGCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG
AGCTGAACAATACTTTACCTGCTTCTTACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTAGAGTGAAACCCACTCACAGGCTTGTCCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTGTTATCCTATTTTGCATGTGTTGAGATCTCAGATCAGTGTGTTTAGAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAA
AAA

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSHL SAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAAHQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATTT
CCTGATGATTTATAGACTCAAAGAAACTCATGTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTTGAAATTT
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGCTGAGG
TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLFLLLISSIYSECKLEIFHFACQWGRSLSLSFYFLKFLQSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC
CGGCCCTCTCCCGCCCCACACCCACCTCCTGGCTCTTCTGTTTTACTCCTCCTTTTCATTTCATA
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGCACTTGATTCTGGTGTTAGTGCTCCCGATTCAAGCTTTCCCCAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT
TGTTGATAACTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGAAGATGTTGATTCAACCAAGAATCGAAACTG
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAAATTTCAAGATGATCCAGATGGTCTTCA
TCACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAATAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGGAGAAAACGATGAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGAAAGGAGAACTAAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTTCAGAAAAAGCAAGAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCCAAGG
GTTATTAGAAAGTCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLTLTNGLE
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK
EEAEAIAKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
GATGGTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAG
CCAGTGCCTGTCTGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCGGCTGCCCTACCCGGGCTGGTTCTGTGCACGGTGCCTGAAGCCGATCAGCC
TGTACAGACTCACCCAGCTTCCCAGAAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACT**TAGGG**CAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
GAGTGGAGGAGACCCATGGCGGACAATCAGTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG
TGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATAAAATTCTGAGATTTGGAGCTCAGT
CCACGGTCTCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGTCT
TAATGGTAAGTGAAGTGTCTACCTGAGCCCCGAGGCCAACCATCCCCAGTTGAGCCTTATA
GGGTGAGTAGCTCTCCACATGAAGTCTGTCTACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA
TGCTACCTTTTCTATCTCTTCCCTCATCATCTGTTGTGGGCATGAGGAGGTGGTGTATGTCAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
GATACAATCAAAATCCCAGATGCTGGTCTCTATTTCCCATGAAAAGTGCTCATGACATATTGAGA
AGACCTACTTACAAAGTGGCATAATATTGCAATTTATTTTAAATTAAGATACCTATTTATATATT
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT
AGGTGATTTTTCTTTAATTCTGTTAATTTATCTGTATTTCTAATTTTTCTACAATGAAGATGA
ATTCTTGTATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAGGAACTTAAAGAACAAAAATCATCTGGTAATTCTTTCTAGAAAG
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAACTCTCAGTCTGTGAGTTTATTTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTGCTGGATGAAGGTAGACCTAAATTCATAT
GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGGAAAGAGGCAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCCGGCTGTTTTAA
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT
CTCCTCGTGTTTACATTCTGTGTGTGTCCCCCTCCACAATGTACCAAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAAGTATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTGCCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAATGAAGTCTCCT
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTTGGTCTAAGTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMDKDSALKVLYLHNNQLLAGGLHAGKVIKGEESVVPNRWLDASLSPVILGVQGGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGAWNAPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGCGCCG
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTCTGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACTTCACCCCTGAAGAAGTCTGTTCCCTCAATCTGATAGGTTT
CAGCCTTATATGCAGGAGGTGGTGCCCTTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACAAAAGGAAGATGGGAAGCCAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTATTGTAAGTGGTGTTC
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCGAGCATGTACCAGGTCAGTGCAGAGGC
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTGCAT
TCTTGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCTAGAGCCTGCTAG
GCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCGT
TGCCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGT
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCAC TTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCCTGTGAAGTGCTGTCTGGAGCAG
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACCTTCTGCACATTTTGAAAAGAG
CAGCTGCTGCTTAGGGCCGCCGGAAGCTGGTGTCTGTCATTTTCTCTCAGGAAAGGTTTTCAAA
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTCCCATCCCCTGCTACCCCTG
GCCCAGCACAGGCACCTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCTGGTTTTATT
TGTTTGT TTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPKQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCCTCTGGTGGTAAATGGACATTTTCCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTCATTGGGGCCCATATATTCCTAATGCAAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAA
AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACA
GTAGAAGTGAACCTTCAACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAAGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCA
GCAGACAAAGTCGTCTTCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTAACTTTTCTGCA
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFNTTTPLGNYMALIQH
STIIGFSQVFEPHQKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPPFLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD
GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCACTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 160

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVMSMRNIESRSTSPWNYTVTWDPNRYPSSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV
RRKHQGCSSVSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG
ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATT
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGTGTCT
TGGCACTGGGCCGAAGCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCTCAGGACGCTACC
CACTGCTCTCCGGGCTCTCCTGCCGCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT
CGTGCCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCC
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA
TGCCCTCTCTCCAGGCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCGCTGCGTCTCTGC
TGGAGGTGCAAGTGCTGTGCCCTTGTGCACTTGTGGTCACTGTGTGGGCTCTGTGGTATATGAC
TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTATACTCAGCCAGGTACGAGAA
GGAATCAACCACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGGTGACA
ACGTGCATCTGGTTCTGAATGTCTGTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG
GTCCAGGGCCCCCAAAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAA
CCACACAGACCTGGTTCCTGCTCTGTATTGAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGA
CGAACATCTGCCCCCTCAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTG
CGACTGCTGACCTGCAGAGCTGGCTGCTGGACGCACCGTGTCTGCTGCCCGCAGAAGCGGCACT
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAAGC
TCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCCTAACCTCTGTGTTCAAGTG
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGTCTGTGGGCTGACTCCCTGGGGCTCTCAAAGA
CGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCA
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTACTA
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCG
CTGCGCTTTCCCTCATCTCTCTCAAAAAGGATCACGCGAAAGGTGGCTGAGGCTCTTGAAA
CAGGACGTCGCGCTCGGGGGCGGGCCAGGGGCGCGCGGCTCTGCTCCTCTACTCAGCCGATGA
CTCGGGTTTCGAGCGCCTGGTGGGCGCCCTGGCGTGGGCCCTGTGCCAGCTGCCGCTGCCGCTGG
CCGTAGACCTGTGGAGCCGTCTGTAAGTGAAGTGAAGCGCAGGGGCCGTGGCTTGGTTTCACGCGCAG
CGGCGCCAGACCCTGCAGGAGGGCGCGGTGGTGGTCTTGTCTCTCTCCCGGTGCCGTGGCGCT
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCGCGGGGCGCACGGCCCGCACGACGCCCTCC
GCGCCTCGCTCAGCTGCGTGTGCCGACTTCTTGACGGCCGGGCGCCCGGAGCTACGTGGG
GCCTGCTTCGACAGGCTGCTCCACCGGACGCCGTACCGCCCTTTTCCGCAACCGTGCCCGTCTT
CACACTGCCCTCCCACTGCCAGACTTCTTGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCG
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTACGCCAGCCCTGGATAGCTACTTC
CATCCCCGGGGACTCCCGCGCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

FIGURE 162

MPVPWFLLSLALGRSPVVLSELRVLVGPQDATHCSPGLSCRLWDSIILCLPGDIVPAPGPVLIAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVNSADGDNVHLVLNV
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLLTLQSWLLDAPCSLPAAEALCWRAPEGDPQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQEQECLWADSLGFLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG
RAALLLYSADDGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGANGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHFDPAVPALFRTVPVFT
LPSQLPDFLGALQQPRAPRSRGLQERAEQVSRALQPALDSYFHPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGA CTGTGGGATCCCTGGCT
 GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
 AGACGTACGGAGAGAGGGGACTGGGTGGCAAAGAAGGGCTGTGACGGGATCACCCGGAAGTCCTGC
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
 GTCAGTGGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA
 CCCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTTGAAGACATCTTCCATGACCTG
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAATGCACCTTGGAGGGAAGCAGAGAGA
 ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCCTTGGCACCATCATGATTTGCGTTCCCA
 CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
 TACTCCTTCTCCGGAGCCTTCTCTGTTCTCCATGGGCTTCTCGTGCAGTACTCTGTACCTGAG
 CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCCCTGACTT
 TCCAGCCGCTGCGCTTCATCCAGGAGCAGTCCCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC
 AGTCTGGCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCTCCAGC
 CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCCAACGCTGCCCTGAG
 GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTCTACGCCCCACA
 GGCCATCTCTAAGTCCAGCCTTCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
 CCTATGGGGTATGCAATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTTAAA
 CACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
 CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGTACACAGTGGGGAGGAAGGGACA
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG
 GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCCTGGCCCTGACTGTGCAGTGGGAGTCCCTG
 AGGGGAATGGGAAAGGCTTGGTGTCTCCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
 ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
 AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCAGGAACAAAGCAGCATGATA
 AGGACTGCAGCGGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGCTGAGCCCTG
 CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAACTCCCAGGTCCAGAGCCCCACCTC
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTGCTCTCCTTGCCCCATTCTGGCCGATTTC
 ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA
 GCCTGGAAAAGAACCAGGCCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAAGAACCTGC
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
 TTCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTAGCTTCATTCTCTGATAGAACAAAGC
 GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTACAGCCCT
 ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC
 TGTACTGATGTACAACTTTGCAAGCTCTGCCTTGGGTTTACGCCATCTGGGCTCAAATTCAGC
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCTCTC
 ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
 TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
 AAAAAAA

FIGURE 164

MRTLITILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTELYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLESMGFLVAVLCYLSYRYVTKPPAP
PNSLNVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFFYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPGQLQKEPPAGSCMLGGLSLQEVTSIAM
EESQEAQSLHQPLGICTDRSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHMSLPLQPPSGPC
SPSDQGPSPWGLLESIVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTVQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCGCGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTGCTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA
AGTGTGTAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAACTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCTGTGCCTGAGCCCAGGCATTCAGAGCTGATTCAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCGCACGATAA
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT
CATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCCAAACAAAAATATATTATTTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFVLGALWWVPGQSDLSHGRRFSDLKVCGDEECSMLMYRGKALEDFTGPDCRFVN
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADETDFVCFEGGRD
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRADESDEGEA
FSESTEGLOQPQAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAACTTC
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAATCCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGCGGCAGGTCCCAGGCCAAGGCGATGCGCGCAGGGGGTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
TCTCGTGTCTGCTGGGCGCCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTTCAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCTCA
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG
TGCCTGCCCAGATCTCTACAGTGGTCTGATGGAAGCAATTCACAGTACCGAAACTGGTACACAG
ATGAACCTTCTGCGGAAGTGAAAAGTGTGTTGTGATGTATCACAACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACCAGTGGAATGATGACAGGTGTAAACATGAAGCACAATTATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAG
GAGACACCCATCAGAAATGTGGTTGTTACTGAAGCAGGTATAATTCCAATCTAATTTATGTTGTT
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT
GCATAAAGTAAAGGAAGAACAATACTAGTCCAAACAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCAGAAATTTGTAATCT
GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAAATCACAAGGATCTGC
AAGATGAAGTGAAGCTCCCCCTTGAGGCAATATTAAAGTAATTTTATATGTCTATTATTTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA
ACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTAGAAGCAATTCCTTTTTATTTCTTTTACCTTTTCATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA
ATGAAGTGTCTAATATTTATTTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAG
AAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTGT
TTTCTCGAAATAATTCATCTTTAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
AATAAGAAGCTATTTTCATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATTTGTGCAAGACATGTGCCTTATAATTATTTTAGCTTAAATTAACAGATT
TTGTAATAATGTAACCTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
TGACATACACAATATAAATCATATGCTTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTCGGGGTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
ACTATATTAGTATACAAAGAGGTCTGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAGGAAGTACGAAATCGTGTGAAAATGGGTTGG
AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTCAAGAGAAAGTTGTAAGTCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTAACCATAAAGAGTCTTGTCTTCTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYKMAVFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRTKTSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-
145, 212-217